```
          10                  30                  50
CACGCGTCCGCGGGCGCGGCCGGAGAACCCCGCAATCTTTGCGCCCACAAAATACACCGA
          70                  90                 110
CGATGCCCGATCTACTTTAAGGGCTGAAACCCACGGGCCTGAGAGACTATAAGAGCGTTC
         130                 150                 170
CCTACCGCCATGGAACAACGGGGACAGAACGCCCCGGCCGCTTCGGGGGCCCGGAAAAGG
           M   E   Q   R   G   Q   N   A   P   A   A   S   G   A   R   K   R
         190                 210                 230
CACGGCCCAGGACCCAGGGAGGCGCGGGGAGCCAGGCCTGGGCCCCGGGTCCCCAAGACC
H   G   P   G   P   R   E   A   R   G   A   R   P   G   P   R   V   P   K   T
         250                 270                 290
CTTGTGCTCGTTGTCGCCGCGGTCCTGCTGTTGGTCTCAGCTGAGTCTGCTCTGATCACC
L   V   L   V   V   A   A   V   L   L   L   V   S   A   E   S   A   L   I   T
         310                 330                 350
CAACAAGACCTAGCTCCCCAGCAGAGAGCGGCCCCACAACAAAAGAGGTCCAGCCCCTCA
Q   Q   D   L   A   P   Q   Q   R   A   A   P   Q   Q   K   R   S   S   P   S
         370                 390                 410
GAGGGATTGTGTCCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGCATCTCCTGC
E   G   L   C   P   P   G   H   H   I   S   E   D   G   R   D   C   I   S   C
         430                 450                 470
AAATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTGCTTGCGCTGCACC
K   Y   G   Q   D   Y   S   T   H   W   N   D   L   L   F   C   L   R   C   T
         490                 510                 530
AGGTGTGATTCAGGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGT
R   C   D   S   G   E   V   E   L   S   P   C   T   T   T   R   N   T   V   C
         550                 570                 590
CAGTGCGAAGAAGGCACCTTCCGGGAAGAAGATTCTCCTGAGATGTGCCGGAAGTGCCGC
Q   C   E   E   G   T   F   R   E   E   D   S   P   E   M   C   R   K   C   R
         610                 630                 650
ACAGGGTGTCCCAGAGGGATGGTCAAGGTCGGTGATTGTACACCCTGGAGTGACATCGAA
T   G   C   P   R   G   M   V   K   V   G   D   C   T   P   W   S   D   I   E
         670                 690                 710
TGTGTCCACAAAGAATCAGGCATCATCATAGGAGTCACAGTTGCAGCCGTAGTCTTGATT
C   V   H   K   E   S   G   I   I   I   G   V   T   V   A   A   V   V   L   I
         730                 750                 770
GTGGCTGTGTTTGTTTGCAAGTCTTTACTGTGGAAGAAAGTCCTTCCTTACCTGAAAGGC
V   A   V   F   V   C   K   S   L   L   W   K   K   V   L   P   Y   L   K   G
         790                 810                 830
ATCTGCTCAGGTGGTGGTGGGGACCCTGAGCGTGTGGACAGAAGCTCACAACGACCTGGG
I   C   S   G   G   G   G   D   P   E   R   V   D   R   S   S   Q   R   P   G
```

FIG. 1A

```
          850                       870                       890
GCTGAGGACAATGTCCTCAATGAGATCGTGAGTATCTTGCAGCCCACCCAGGTCCCTGAG
A  E  D  N  V  L  N  E  I  V  S  I  L  Q  P  T  Q  V  P  E
          910                       930                       950
CAGGAAATGGAAGTCCAGGAGCCAGCAGAGCCAACAGGTGTCAACATGTTGTCCCCCGGG
Q  E  M  E  V  Q  E  P  A  E  P  T  G  V  N  M  L  S  P  G
          970                       990                      1010
GAGTCAGAGCATCTGCTGGAACCGGCAGAAGCTGAAAGGTCTCAGAGGAGGAGGCTGCTG
E  S  E  H  L  L  E  P  A  E  A  E  R  S  Q  R  R  R  L  L
         1030                      1050                      1070
GTTCCAGCAAATGAAGGTGATCCCACTGAGACTCTGAGACAGTGCTTCGATGACTTTGCA
V  P  A  N  E  G  D  P  T  E  T  L  R  Q  C  F  D  D  F  A
         1090                      1110                      1130
GACTTGGTGCCCTTTGACTCCTGGGAGCCGCTCATGAGGAAGTTGGGCCTCATGGACAAT
D  L  V  P  F  D  S  W  E  P  L  M  R  K  L  G  L  M  D  N
         1150                      1170                      1190
GAGATAAAGGTGGCTAAAGCTGAGGCAGCGGGCCACAGGGACACCTTGTACACGATGCTG
E  I  K  V  A  K  A  E  A  A  G  H  R  D  T  L  Y  T  M  L
         1210                      1230                      1250
ATAAAGTGGGTCAACAAAACCGGGCGAGATGCCTCTGTCCACACCCTGCTGGATGCCTTG
I  K  W  V  N  K  T  G  R  D  A  S  V  H  T  L  L  D  A  L
         1270                      1290                      1310
GAGACGCTGGGAGAGAGACTTGCCAAGCAGAAGATTGAGGACCACTTGTTGAGCTCTGGA
E  T  L  G  E  R  L  A  K  Q  K  I  E  D  H  L  L  S  S  G
         1330                      1350                      1370
AAGTTCATGTATCTAGAAGGTAATGCAGACTCTGCCATGTCCTAAGTGTGATTCTCTTCA
K  F  M  Y  L  E  G  N  A  D  S  A  M  S  *
         1390                      1410                      1430
GGAAGTGAGACCTTCCCTGGTTTACCTTTTTTCTGGAAAAAGCCCAACTGGACTCCAGTC
         1450                      1470                      1490
AGTAGGAAAGTGCCACAATTGTCACATGACCGGTACTGGAAGAAACTCTCCCATCCAACA
         1510                      1530                      1550
TCACCCAGTGGATGGAACATCCTGTAACTTTTCACTGCACTTGGCATTATTTTTATAAGC
         1570                      1590
TGAATGTGATAATAAGGACACTATGGAAAAAAAAAAAAA
```

FIG. 1B

```
1   M - L G - - - - - - - - - - - - - - - - - - - - - - - - - - - I W T L L P L V L   h Fas protein
1   M G L S - - - - - - - - - - - - - - - - - - - - - - - - - - - T V P D L L L P L   h TNFR I Protein
1   M E Q R - - - - - - - - - - - - - - - - - - - - - - - - - - - P R G C A A V A A   DR3 protein
1   M E Q R G Q N A P A A S G A R K R H G P G P R E A R G A R P G P R V P K T L V L   HLYBX88XXprotein

13  T S V A R L S S K S V N A Q V T D I N S K G L E L R K T V T T V E T Q N L E G L   h Fas protein
14  V L L E L L V G I Y P S G V I G L V P H L G D R E K R D S V C P Q G K Y I H - -   h TNFR I Protein
14  A L L L V L L G A R A Q G - - - - - - - - G T R S P R - C D C A - G D F - H - -   DR3 protein
41  V V A A V L L L V S A E S A L I T Q Q D L A P Q Q R A A P Q Q K R S S P S E G L   HLYBX88XXprotein

53  H H D G Q F C H K P C P P G E R K A R D C T V N G D E P D C V P C Q E G K E Y T   h Fas protein
52  P Q N N S I C C T K C H K G T Y L Y N D C P G P G Q D T D C R E C E S G S F T A   h TNFR I Protein
41  K K I G L F C C R G C P A G H Y L K A P C T E P C G N S T C L V C P Q D T F L A   DR3 protein
81  - - - - - - - - - - C P P G H H I S E D - - - - - - G R D C I S C K Y G Q D Y S   HLYBX88XXprotein

93  D K A H F S S K C R R C R L C D E G H G L E V E I N C T R T Q N T K C R C K P N   h Fas protein
92  S E N H L R - H C L S C S K C R K E M G Q V E I S S C T V D R D T V C G C R K N   h TNFR I Protein
81  W E N H H N S E C A R C Q A C D E Q A S Q V A L E N C S A V A D T R C G C K P G   DR3 protein
105 T H W N D L L F C L R C T R C D - - S G E V E L S P C T T T R N T V C Q C E E G   HLYBX88XXprotein

133 F F - - - - - - - - - - C N S T V - - - C E H C D P C T K - - - - - - - - - - -   h Fas protein
131 Q Y R H Y W S E N L F Q C - - - - - F N C S L C L N - G T V H - - - - L S C Q E   h TNFR I Protein
121 W F V E C - - - Q V S Q C V S S S P F Y C Q P C L D C G A L H R H T R L L C S R   DR3 protein
143 T F R E - - - - - - - - - - E D S P E M C R K C - - - - - - - - - - R T G C P R   HLYBX88XXprotein
```

FIG.2A

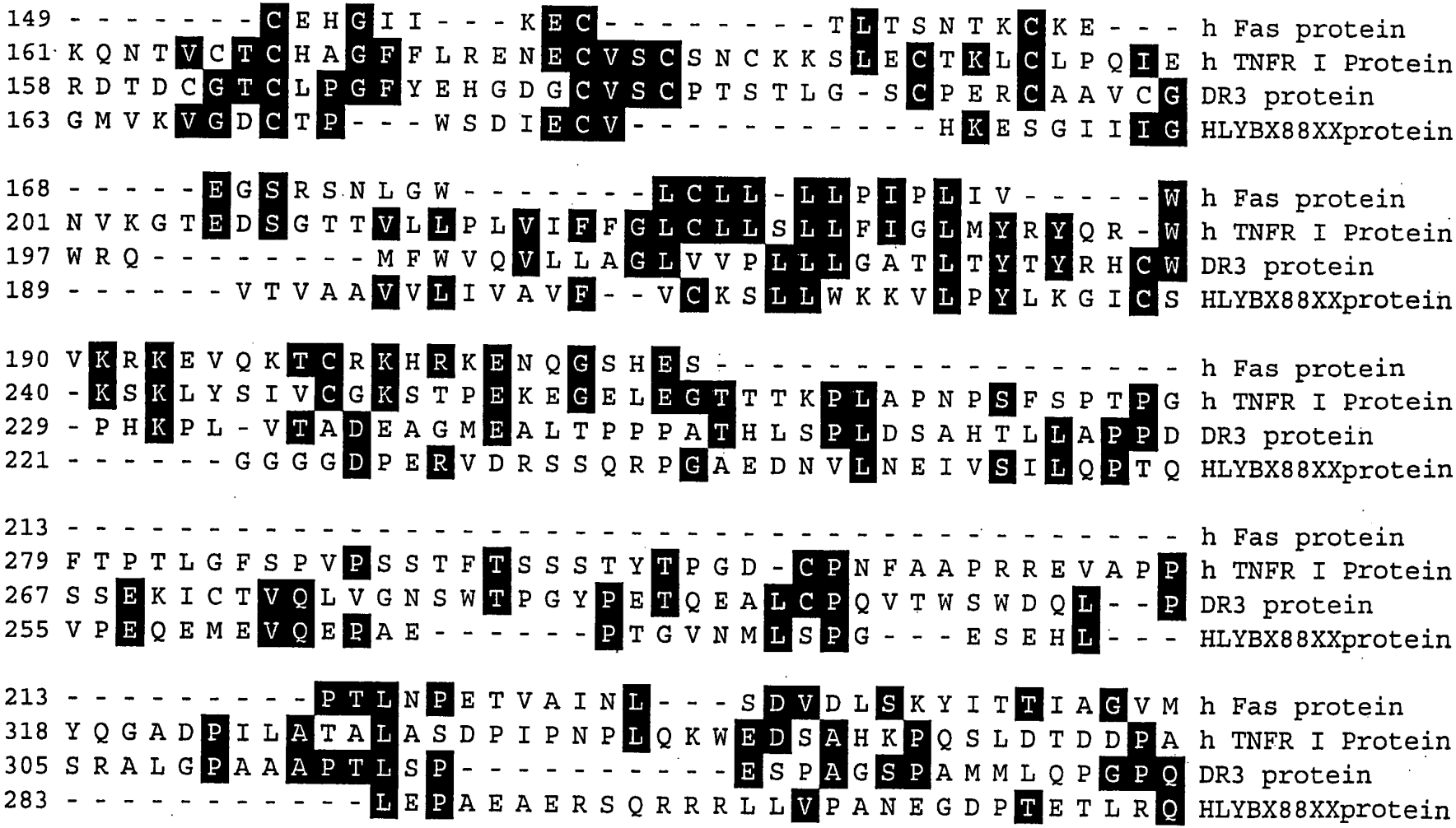

149 - - - - - - - C E H G I I - - - K E C - - - - - - - - - T L T S N T K C K E - - - h Fas protein
161 K Q N T V C T C H A G F F L R E N E C V S C S N C K K S L E C T K L C L P Q I E h TNFR I Protein
158 R D T D C G T C L P G F Y E H G D G C V S C P T S T L G - S C P E R C A A V C G DR3 protein
163 G M V K V G D C T P - - - W S D I E C V - - - - - - - - - - - - H K E S G I I I G HLYBX88XXprotein
168 - - - - - E G S R S N L G W - - - - - - - L C L L - L L P I P L I V - - - - - W h Fas protein
201 N V K G T E D S G T T V L L P L V I F F G L C L L S L L F I G L M Y R Y Q R - W h TNFR I Protein
197 W R Q - - - - - - - - - M F W V Q V L L A G L V V P L L L G A T L T Y T Y R H C W DR3 protein
189 - - - - - - V T V A A V V L I V A V F - - V C K S L L W K K V L P Y L K G I C S HLYBX88XXprotein
190 V K R K E V Q K T C R K H R K E N Q G S H E S - - - - - - - - - - - - - - - - - - h Fas protein
240 - K S K L Y S I V C G K S T P E K E G E L E G T T T K P L A P N P S F S P T P G h TNFR I Protein
229 - P H K P L - V T A D E A G M E A L T P P P A T H L S P L D S A H T L L A P P D DR3 protein
221 - - - - - - G G G G D P E R V D R S S Q R P G A E D N V L N E I V S I L Q P T Q HLYBX88XXprotein
213 - h Fas protein
279 F T P T L G F S P V P S S T F T S S S T Y T P G D - C P N F A A P R R E V A P P h TNFR I Protein
267 S S E K I C T V Q L V G N S W T P G Y P E T Q E A L C P Q V T W S W D Q L - - P DR3 protein
255 V P E Q E M E V Q E P A E - - - - - - P T G V N M L S P G - - - E S E H L - - - HLYBX88XXprotein
213 - - - - - - - - - - P T L N P E T V A I N L - - - S D V D L S K Y I T T I A G V M h Fas protein
318 Y Q G A D P I L A T A L A S D P I P N P L Q K W E D S A H K P Q S L D T D D P A h TNFR I Protein
305 S R A L G P A A A P T L S P - - - - - - - - - - - E S P A G S P A M M L Q P G P Q DR3 protein
283 - - - - - - - - - - - - - L E P A E A E R S Q R R R L L V P A N E G D P T E T L R Q HLYBX88XXprotein

FIG.2B

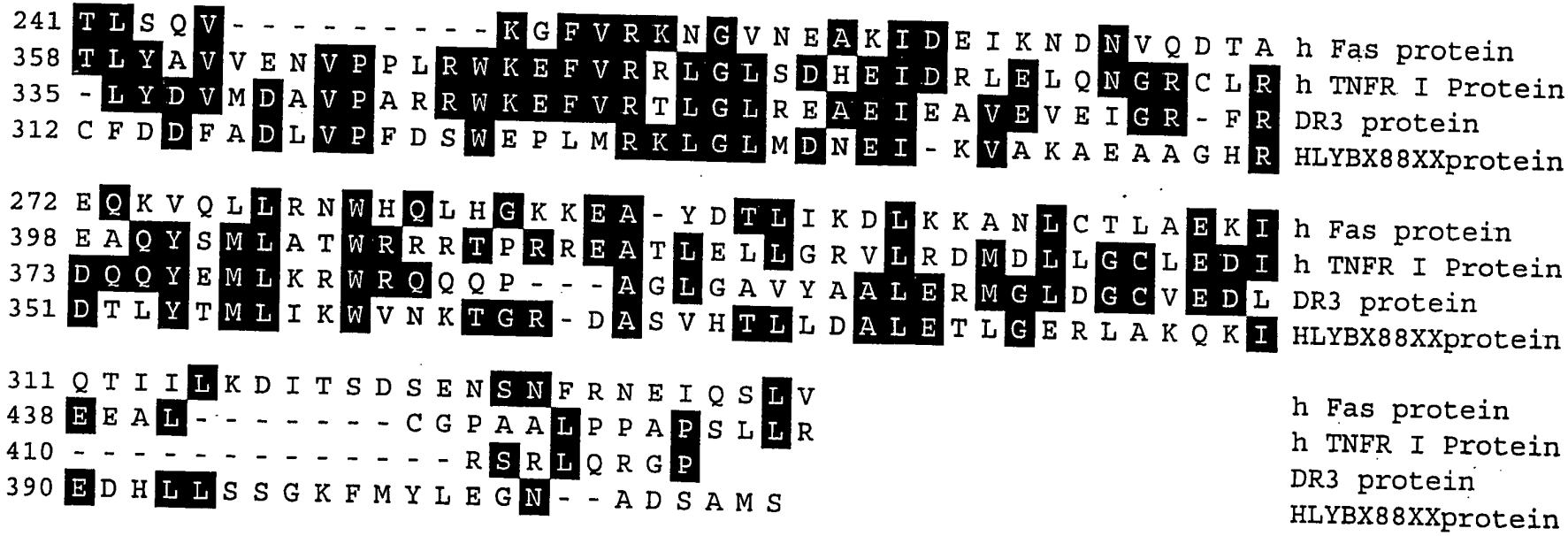

241 TLSQV----------KGFVRKNGVNEAKIDEIKNDNVQDTA h Fas protein
358 TLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGRCLR h TNFR I Protein
335 -LYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FR DR3 protein
312 CFDDFADLVPFDSWEPLMRKLGLMDNEI-KVAKAEAAGHR HLYBX88XXprotein
272 EQKVQLLRNWHQLHGKKEA-YDTLIKDLKKANLCTLAEKI h Fas protein
398 EAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDI h TNFR I Protein
373 DQQYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVEDL DR3 protein
351 DTLYTMLIKWVNKTGR-DASVHTLLDALETLGERLAKQKI HLYBX88XXprotein
311 QTIILKDITSDSENSNFRNEIQSLV h Fas protein
438 EEAL-------CGPAALPPAPSLLR h TNFR I Protein
410 ----------RSRLQRGP DR3 protein
390 EDHLLSSGKFMYLEGN--ADSAMS HLYBX88XXprotein

FIG.2C

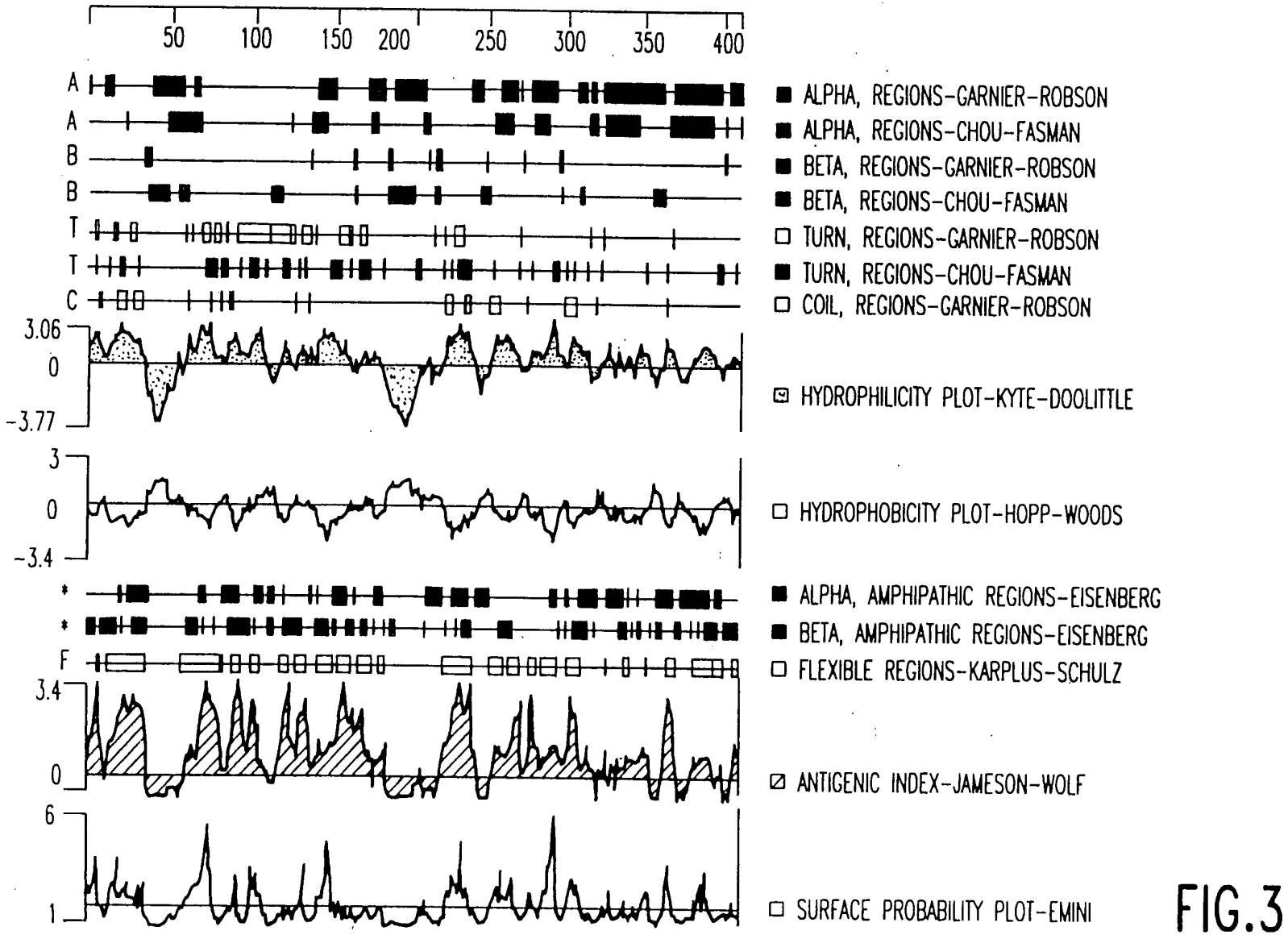

50
100
150
200
250
300
350
400
A
A
B
B
T
T
C
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
3.06
0
-3.77
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
3
0
-3.4
HYDROPHOBICITY PLOT-HOPP-WOODS
*
*
F
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
3.4
0
ANTIGENIC INDEX-JAMESON-WOLF
6
1
SURFACE PROBABILITY PLOT-EMINI

FIG.3

HAPBU13R

```
  1 AATTCGGCAC AGCTCTTCAG GAAGTCAGAC CTTCCCTGGT TTACCTTTTT
 51 TCTGGAAAAA GCCCAACTGG GACTCCAGTC AGTAGGAAAG TGCCACAATT
101 GTCACATGAC CGGTACTGGA AGAAACTCTC CCATCCAACA TCACCCAGTG
151 GNATGGGAAC ACTGATGAAC TTTTCACTGC ACTTGGCATT ATTTTTGTNA
201 AGCTGAATGT GATAATAAGG GCACTGATGG AAATGTCTGG ATCATTCCGG
251 TTGTGCGTAC TTTGAGATTT GNGTTTGGGG ATGTNCATTG TGTTTGACAG
301 CACTTTTTTN ATCCCTAATG TNAAATGCNT NATTTGATTG TGANTTGGGG
351 GTNAACATTG GTNAAGGNTN CCCNTNTGAC ACAGTAGNTG GTNCCCGACT
401 TANAATNGNN GAANANGATG NATNANGAAC CTTTTTTTGG GTGGGGGGGT
451 NNCGGGGCAG TNNAANGNNG NCTCCCCAGG TTTGGNGTNG CAATNGNGGA
501 ANNNTGG
```

HSBBU76R

```
  1 TTTTTTTTGT AGATGGATCT TACAATGTAG CCCAAATAAA TAAATAAAGC
 51 ATTTACATTA GGATAAAAAA GTGCTGTGAA AACAATGACA TCCCAAACCA
101 AATCTCAAAG TACGCACAAA CGGAATGATC CAGACATTTC CATAGNGTCC
151 TTATTATCAC ATTCAGCTTA TAAAANTAAT GCCAAGTGCA GTGAAAAGTT
201 ACAGGATGTT CCATCCACTG GGTGGATT
```

FIG.4

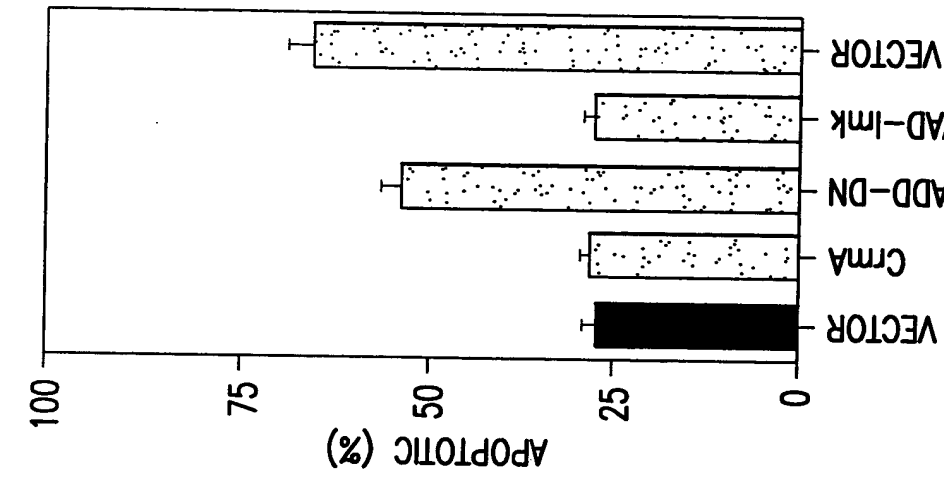


FIG. 5C

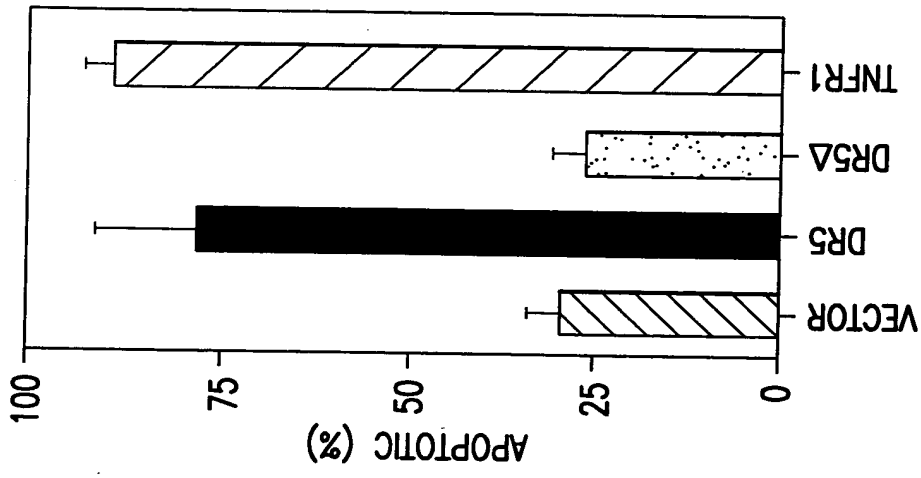


FIG. 5B

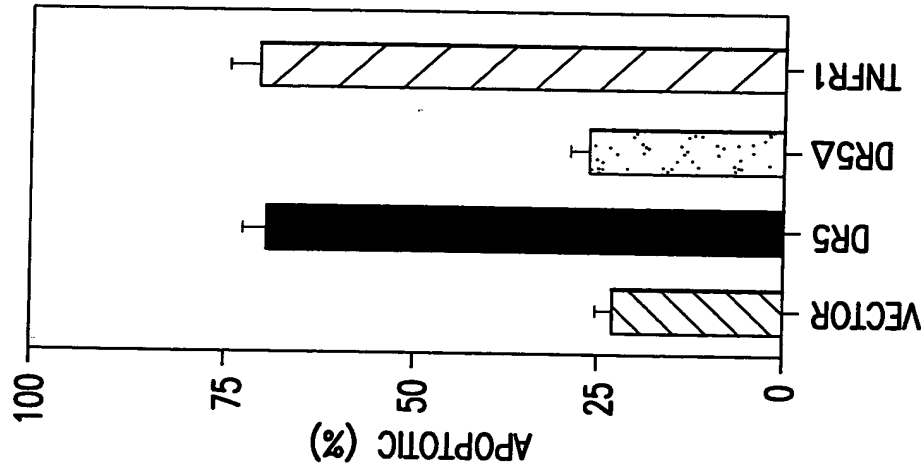


FIG. 5A

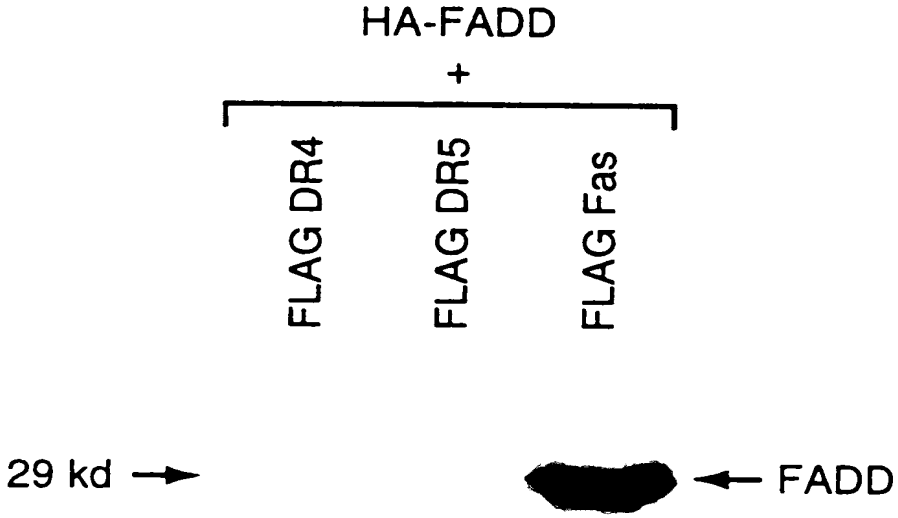
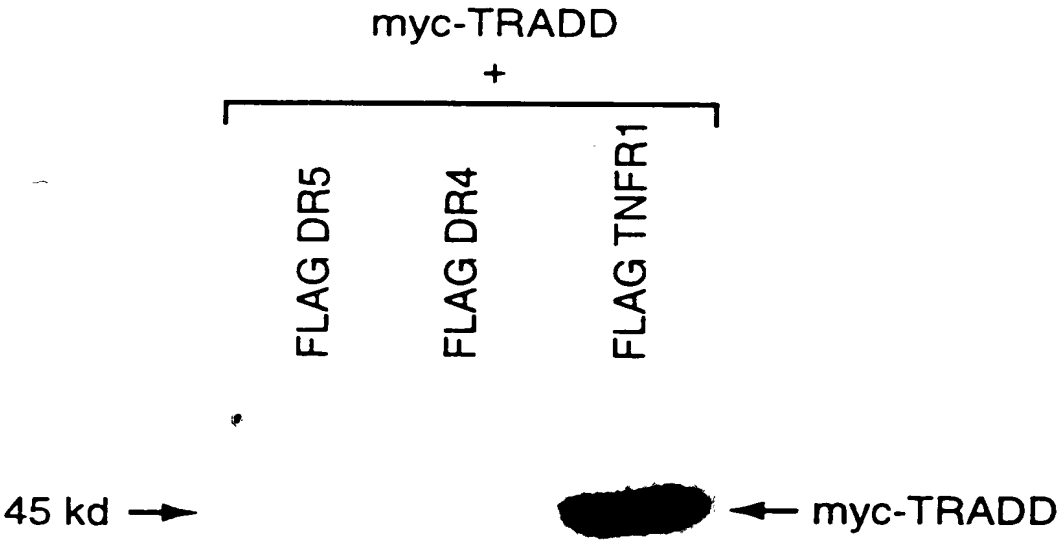

HA-FADD
+
FLAG DR4
FLAG DR5
FLAG Fas
29 kd
FADD

FIG.5D


myc-TRADD
+
FLAG DR5
FLAG DR4
FLAG TNFR1
45 kd
myc-TRADD

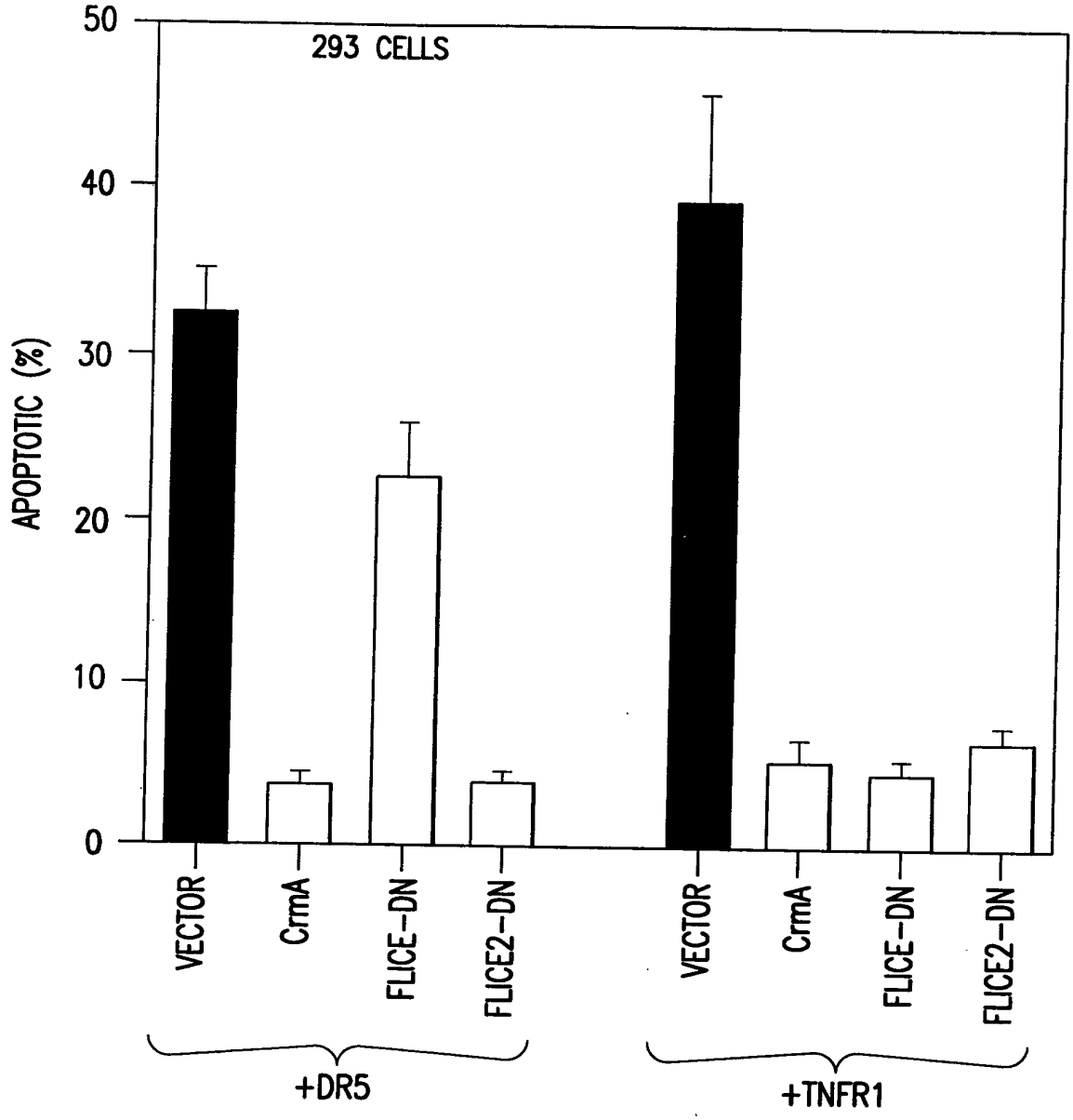
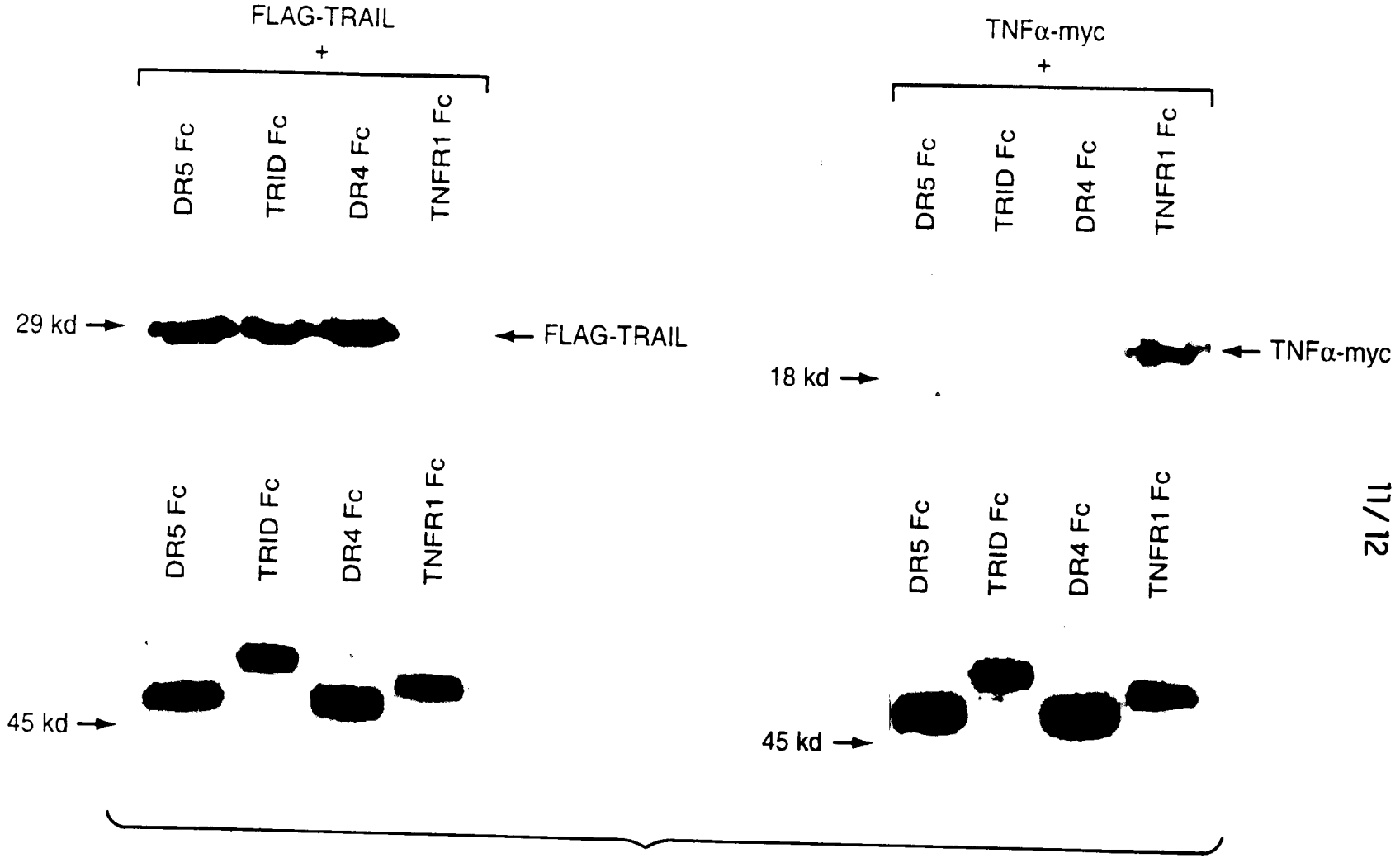

293 CELLS
APOPTOTIC (%)
50
40
30
20
10
0
VECTOR
CrmA
FLICE-DN
FLICE2-DN
VECTOR
CrmA
FLICE-DN
FLICE2-DN
+DR5
+TNFR1

FIG. 5E


FLAG-TRAIL
+
DR5 Fc
TRID Fc
DR4 Fc
TNFR1 Fc
29 kd
FLAG-TRAIL
TNFα-myc
+
DR5 Fc
TRID Fc
DR4 Fc
TNFR1 Fc
18 kd
TNFα-myc
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DR4 Fc
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45 kd
DR5 Fc
TRID Fc
DR4 Fc
TNFR1 Fc
45 kd

FIG.6A

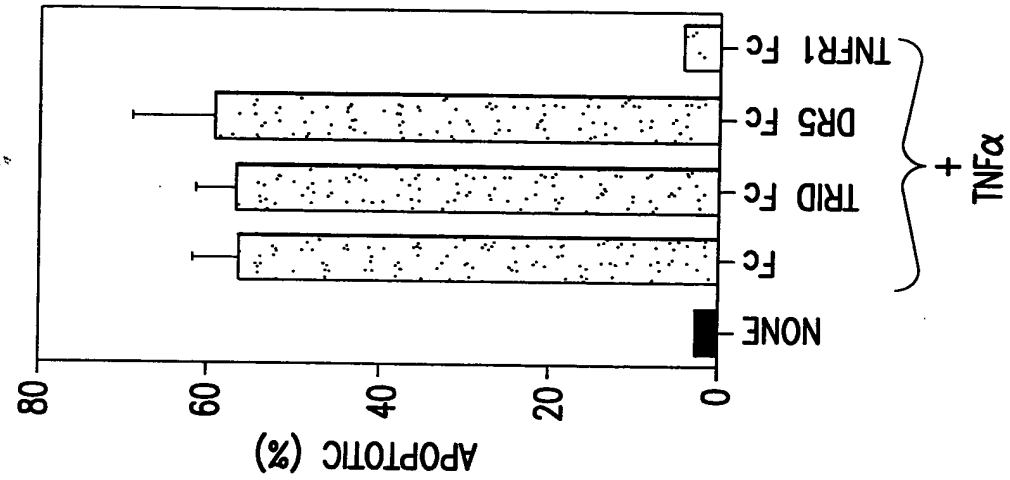
APOPTOTIC (%)
0
20
40
60
80
NONE
Fc
TRID Fc
DR5 Fc
TNFR1 Fc
+
TNFα

FIG. 6C

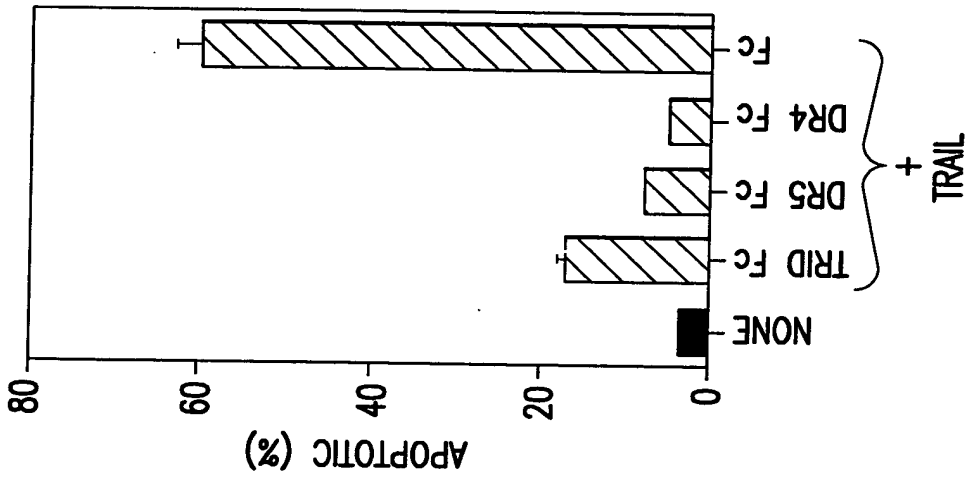
APOPTOTIC (%)
0
20
40
60
80
NONE
TRID Fc
DR5 Fc
DR4 Fc
Fc
+
TRAIL

FIG. 6B